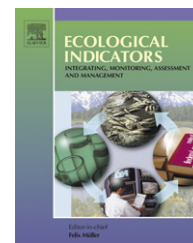


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Developing SSU rDNA metagenomic profiles of aquatic microbial communities for environmental assessments

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ABSTRACT

Five water samples from three sources, two municipal reservoirs in central North Carolina and Toolik Lake in Alaska, were processed to conduct a comparative survey of microbial small subunit rDNA sequences. Genomic DNA was extracted and amplified by PCR using universal SSU rDNA primers to generate 16S and 18S rDNA clone libraries and 50 clones from each library were sequenced and placed in operational taxonomic units (OTUs). Through this recovery and analysis of SSU rRNA genes, a metagenomic profile of the microbial community emerged for each environmental sample. Analyses of these profiles, including species diversity estimates and rank-abundance curves, revealed that approximately 64% of prokaryotic OTUs and 80% of eukaryotic OTUs were novel. Diversity estimates were consistent with predicted ecosystem characteristics: they were greater for the mesotrophic to eutrophic temperate lakes, than for the oligotrophic arctic lake. Sample comparisons showed that community similarity declined as geographic distance between sites increased. Real-time quantitative PCR results showed that OTUs which had been recovered from only one library were actually present in other samples, but at much lower frequencies, suggesting that many, if not most, microorganisms are cosmopolitan. Together, these results support the potential value of using the microbial community as an indicator of local environmental conditions. In other words, it may be realistic to monitor water quality using a single, comprehensive suite of microorganisms by analyzing patterns of relative abundance.

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1. Introduction

Molecular approaches have great potential for comprehensive environmental assessments of aquatic microbial communities (Devereux et al., 2006; von Mering et al., 2007). This potential derives from several methodological characteristics, which allow for more thorough assessments of microbial communities than non-molecular methods. The greater

sensitivity and specificity provided by molecular assays are advantages that have become well-known through studies that employ techniques like PCR and real-time PCR to target single taxa in environmental samples (e.g. Bowers et al., 2000; Wilson et al., 2000). With molecular approaches, it is also possible to generate libraries of cloned DNA, such as prokaryotic or eukaryotic small subunit ribosomal RNA genes (SSU rDNA), which have illuminated the extensive diversity of

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known and novel taxa in aquatic systems (e.g. Crump et al., 2003). Finally, the development of microarray technologies (e.g. Castiglioni et al., 2004) holds promise for assessing multiple targets in a single assay.

The value of these molecular technologies in comprehensive environmental assessments also relies on the well-known linkage between environmental parameters and the presence of specific microbial taxa. For example, there are seasonal changes in phytoplankton taxa in arctic and temperate lakes, such as cryptophyte dominance under winter ice, followed by spring diatom blooms and dominance by green algae and cyanobacteria during warmer summer months (e.g. Wetzel, 1983). Other studies have shown that lake bacterial communities shift in response to changes in organic matter source (Lindström, 2001; Crump et al., 2003) and the abundance of algal taxa (Lindström, 2001). Callieri and Stockner (2002) have noted that autotrophic picoplankton (0.2–2 µm) communities change across trophic, temperature, and phosphorus concentration gradients in lakes. Since microbial taxa generally have short generation times and high metabolic rates, they can be viewed as rapid and sensitive biological indicators of environmental change. Such change may be monitored at the cellular level as ribosomal RNA gene transcription is either up- or down-regulated. However, rDNA also provides an environmental signal since microbial populations constantly fluctuate in response to changing conditions, and rDNA is generally a reflection of cell abundance. It is also easier to extract and purify DNA than RNA from natural samples without degradation. Thus, a profile of microbial community rDNAs should reflect the character of the surrounding environment.

Generally, molecular methods have been used to determine the presence or abundance of single species or limited taxonomic groups, or to assess taxonomic diversity qualitatively in natural systems. For example, ribosomal RNA genes have been used for the identification of microbial taxa (e.g. Pace et al., 1986; Ward et al., 1990; Amann et al., 1995). In recent years, this approach has been expanded to characterize a largely unknown composite of microbial genomes represented in environmental samples. An unexpected level of species diversity has been recovered from marine samples using 16S rRNA genes and whole-genome shotgun cloning methods (Giovannoni et al., 1990; Venter et al., 2004; Sogin et al., 2006). Samples from the Antarctic polar front and equatorial Pacific Ocean have shown high levels of eukaryotic diversity based on 18S rDNA sequences (López-García et al., 2001; Moon-van der Staay et al., 2001; Venter et al., 2004). Similar approaches have revealed a considerable number of unidentified prokaryotes and eukaryotes in freshwater sources (e.g. Bahr et al., 1996; Zwart et al., 1998; Glöckner et al., 2000; Crump et al., 2003), confirming that most microbial species are not routinely cultured (Ward et al., 1990; Torsvik et al., 2002).

Changes in prokaryotic communities related to physical, chemical, and biological characteristics of aquatic systems have also been demonstrated using molecular methods (e.g. Methé and Zehr, 1999; Van Hanne et al., 1999; Casamayor et al., 2002; Crump et al., 2003; Fawley et al., 2004). Characterizations of rDNAs drawn from marine samples have even revealed that the microbial community profile is highly

predictable for a given collection location and time of year (Fuhrman et al., 2006). These studies also raise intriguing questions concerning the distribution limits of microorganisms because taxa have often been detected in unexpected places. For example, the SAR11 cluster, an SSU rRNA gene cluster believed to represent a group of uncultured α -Proteobacteria, has been found in both oceanic systems and arctic freshwater lakes (Giovannoni et al., 1990; Bahr et al., 1996). In fact, several recent papers have discussed the possibility that microbial species are globally distributed (e.g. Zwart et al., 1998, 2002; Finlay, 2002; Fenchel, 2003; Papke et al., 2003; Whitaker et al., 2003).

Exhaustive characterizations of species richness may ultimately demonstrate that “everything microbial is everywhere”, but this approach often overlooks important quantitative data. Metagenomic profiles, however, encompass both qualitative and quantitative aspects of diversity, which are essential for a substantial environmental characterization. In this study, our primary objective was to evaluate whether metagenomic profiling can be used as an ecosystem assessment tool. To do so, we compared five metagenomic profiles of three aquatic systems by evaluating the sequence information generated from a relatively small number of clones taken from rDNA clone libraries. We also determined if patterns of sample complexity and similarity followed generally acknowledged ecological precepts.

2. Materials and methods

2.1. Definition

As used in this paper, the term “metagenomic profile” refers to the DNA sequences that are recovered and analyzed to characterize the pool of genomes present in a sample. In this study, profiles are based on the recovery and analysis of SSU rDNA sequences from prokaryotic and eukaryotic microbes.

2.2. Water samples

Three lakes were sampled in this study: Lake Townsend (36°11'N, 79°43'W, Greensboro, NC); City Lake (35°59'N, 79°56'W, High Point, NC); Toolik Lake (68°38'N, 149°43'W, Alaska). Lake Townsend and City Lake are temperate mesotrophic and eutrophic municipal drinking water reservoirs, respectively. Toolik Lake is a highly oligotrophic, glacial lake located within the Arctic Long Term Ecological Research (LTER) Site above the Arctic Circle in Alaska (O'Brien et al., 1997; <http://ecosystems.mbl.edu/ARC/>). Three Lake Townsend samples were collected: two pelagic surface water samples collected at the same location on 14 June 2000 and 28 March 2001, and a near-shore sample also collected on 14 June 2000. A third pelagic sample was collected from City Lake, an artificially aerated reservoir, near a subsurface water treatment system intake on 22 May 2001. The fourth pelagic sample was collected from Toolik Lake near the main LTER sampling station on 11 August 2000. Each sample (~100 ml) was drawn through a GF/C glass fiber filter that was placed in CTAB buffer for storage at room temperature until later DNA extraction.

2.3. DNA extraction

Genomic DNA was extracted from each water sample using a CTAB (cetyltrimethylammonium bromide) buffer DNA isolation technique (Schaefer, 1997). Briefly, the glass fiber filter was macerated in 2 ml CTAB using a sterile wooden applicator stick. The mixture was heated for 1 h at 65 °C, then mixed with 2 ml 24:1 (v/v) chloroform–isoamyl alcohol by inverting several times and then centrifuged. The aqueous portion was transferred to a 1.5 ml tube, 0.7 volumes of 100% 2-propanol were added, and the tube mixed by inverting several times. The precipitate was pelleted by centrifugation at 14,000 rpm for 25 min at room temperature, the supernatant decanted, and the DNA pellet air-dried. The pellet was then rehydrated in 25 µl TE buffer (pH 7.4) and stored at –20 °C.

2.4. PCR amplification and verification

Prokaryotic and eukaryotic SSU rDNA were amplified by PCR in separate 50 µl reactions using 16S and 18S forward and reverse primers (Table 1) that complement universally conserved regions of SSU rDNA in prokaryotes and eukaryotes (Medlin et al., 1988; Edwards et al., 1989). Each reaction included the following: 5 µl 10× PCR Buffer; 5 µl Promega 25 mM MgCl₂; 5 µl 100 mM BSA; 2.5 µl 16 mM dNTP stock (4 mM each of dATP, dCTP, dGTP and dTTP); 1 µl each of 10 µM forward and reverse primers; 1 U Taq DNA Polymerase; 30.2 µl sterile deionized H₂O; 1 µl genomic DNA (~25 ng). An MJ Research PTC-100 Programmable Thermal Controller was used to execute the following conditions for amplification: initial 2 min denaturation at 94 °C; 30 cycles—1 min denaturation at 94 °C, 1 min annealing at 56 °C for 16S primers or 58 °C for 18S primers, and 2 min extension at 72 °C; final 5 min extension at 72 °C. PCR products were verified by gel electrophoresis.

2.5. Cloning and sequencing

Clones from each PCR product were produced using the Invitrogen TOPO TA Cloning Kit according to the manufacturer's protocol. First, ligation reactions were prepared in which verified PCR products were subcloned en masse into the pCR® 4-TOPO® plasmid vector. Reaction mixtures were then used to transform TOP10 Chemically Competent *E. coli* cells and transformants containing recombinant plasmids were identified by the formation of bacterial colonies on LB agar

plates containing 50 µg/ml ampicillin. This process eliminates the need to screen recombinants from non-recombinants because a lethal fusion gene is expressed in non-recombinants, resulting in cell death. In contrast, recombinants are able to survive due to the presence of a PCR amplicon insert, which interrupts the lethal gene. Individual colonies were inoculated into LB liquid medium containing 50 µg/ml ampicillin and cultured overnight with antibiotic selection. Purified plasmid DNA from each overnight culture was recovered using a Qiagen QIAprep Spin Miniprep Kit according to the manufacturer's protocol.

In summary, each lake sample was used to prepare separate PCR reactions for the amplification of 16S rDNA and 18S rDNA. Each PCR reaction product was used to construct a library of clones, each of which corresponded to a single SSU rDNA amplicon. Finally, restriction digests and gel electrophoresis were performed to verify the presence of a DNA fragment corresponding in size to 16S rDNA or 18S rDNA in each clone.

A LI-COR Global Edition IR² System for automated DNA sequencing was used to generate sequences for fifty verified clones from each library. Comparative analyses of these sequences were performed so that clones could be sorted into artificial groups as a means to investigate microbial communities within and between samples. Sequencing reactions were prepared using an Epicentre Technologies SequiTherm EXCEL™ II DNA Sequencing Kit-LC (for 25–41 cm gels) according to the Cycle Sequencing Protocol provided. Sequencing reactions included: 3.5× SequiTherm EXCEL II Sequencing Buffer; IRD-labeled M13-20 forward and reverse primers; purified 16S rDNA or 18S rDNA; sterile deionized H₂O; SequiTherm EXCEL II DNA Polymerase; SequiTherm EXCEL II-LC Termination Mixes A, C, G and T (each containing dATP, dCTP, dTTP, 7-deaza-dGTP, and one ddNTP). Using an MJ Research PTC-100 Programmable Thermal Controller, reactions were amplified by PCR using the following conditions: initial 4.5 min denaturation at 95 °C; 30 cycles of 30 s denaturation at 95 °C, 30 s annealing at 51 °C, and 1 min extension at 70 °C. After amplification, Stop/Loading Buffer was added to each reaction, which was then denatured for 5 min at 95 °C and loaded into a 41 cm polyacrylamide gel. During electrophoresis of the reaction products, dual 700 and 800 nm detection channels were used simultaneously to generate bidirectional sequences which were at least 550 nucleotides (nt) in each direction.

2.6. Sequence alignments and community analyses

Partial sequences, consisting of the first 500 nt from both 5' and 3' ends, were obtained for each clone and used in subsequent data analyses. 1000 nt of sequence data provide sufficient information for a detailed phylogenetic analysis (Pace et al., 1986). For comparison, we also generated complete 18S rDNA sequences in a later examination and obtained the same results. All sequences were submitted to CHIMERA_-CHECK (Version 2.7; Ribosomal Database Project II, Center for Microbial Ecology, Michigan State University [<http://rdp.cme.msu.edu/html/analyses.html>]), a program designed to detect the presence of chimeric properties, so that PCR artifacts could be identified and eliminated. Based on this

Table 1 – Sequences and target positions of primers used in this study

Primer	Sequence	Location
16S forward	AGAGTTTGATCCTGGCTCAG ^a	8–27 ^b
16S reverse	AAGGAGGTGATCCAGCCGCA ^a	1541–1522 ^b
18S forward	AACCTGTTGATCCTGCCAGT ^c	1–21 ^d
18S reverse	TGATCCTTCTGCAGGTTACCTAC ^c	1795–1772 ^d

^a Primers from Edwards et al. (1989) and Bruce et al. (1992).

^b Position in *E. coli* (Brosius et al., 1981).

^c Primers from Medlin et al. (1988).

^d Position in *S. cerevisiae* (Rubstov et al., 1980).

inspection, only one 16S rDNA clone appeared to be chimeric and was excluded from further consideration. All remaining sequences were submitted to the National Center for Biotechnology Information for BLAST analysis (Altschul et al., 1990 [<http://www.ncbi.nlm.nih.gov/>]), a web-based program that was used to compare each clone sequence to reported sequences in the GenBank database. The results were used to determine whether or not each clone should be characterized as novel.

Sequence alignments and taxonomic analyses were performed using the BioEdit Sequence Alignment Editor and Analysis software (Version 5.0.9; Department of Microbiology, North Carolina State University [<http://www.mbio.ncsu.edu/BioEdit/bioedit.html>]), which includes CLUSTAL W as an accessory application for multiple alignments. Briefly, the CLUSTAL W basic multiple alignment algorithm performs three primary functions (Thompson et al., 1994). First, pairwise alignments of all sequences are generated and used to calculate a distance matrix giving the divergence of each pair of sequences. Second, the distance matrix is used to compute a guide tree, and third, the branching order of the tree is used to align the sequences progressively. In this study, sequences within each library were initially aligned for comparison with each other. Sequences from two libraries were then combined and aligned for pairwise sample comparisons (100 sequences of 16S rDNA or 18S rDNA). Finally, all sequences were combined for group comparisons using all 249 16S rDNA sequences and all 250 18S rDNA sequences.

Taxonomic analyses were performed using the BioEdit sequence identity matrix application, which executes a pairwise comparison of all sequences submitted and calculates the proportion of identical nucleotides between each pair. Clone sequences that returned an identity score of 0.975 or higher, indicating at least 97.5% similarity, were grouped together, while any remaining sequences were grouped alone. This similarity threshold results in groupings, or operational taxonomic units (OTUs), which generally correspond to the species level (Godon et al., 1997; Schloss and Handelsman, 2005). By definition, OTUs with only one clone (“unique OTUs”) occurred when a sequence was less than 97.5% similar to every other sequence in the library.

After grouping clones into OTUs, several diversity indices were calculated for each library. These included: (1) species richness, or the total number of OTUs; (2) evenness, or Simpson’s dominance index, which measures the distribution of clones among OTUs; (3) the Shannon–Wiener diversity index, a statistic used to measure the probability of correctly guessing the OTU identity of a randomly selected clone (Colinvaux, 1993). In addition, Sorenson similarity coefficients (Lincoln et al., 1998) were calculated to measure community similarity, or the proportion of OTUs shared by two libraries.

We also estimated total species richness (S) using four methods based on the distribution of OTUs within a library. These included: S_{cov} , an estimate based on “coverage” (Good, 1953; Giovannoni et al., 1990); S_{max} , an estimate based on rarefaction analysis (Hurlbert, 1971; Nübel et al., 1999) which was performed using the program Analytic Rarefaction (Version 1.3; Stratigraphy Lab, University of Georgia [<http://www.uga.edu/~strata/software/>]); S_{ACE} and S_{Chao1} , two esti-

mates that were evaluated using a form processor and spreadsheet available through a web-based interface (<http://www.aslo.org/lomethods/free/2004/0114a.html>).

Coverage uses the diversity profile of a subsample to estimate the fraction of actual diversity recovered from a sample of infinite size (Good, 1953; Giovannoni et al., 1990; Ravensschlag et al., 1999). S_{cov} projects a total species number based on this proportion. In a rarefaction analysis, species richness and relative abundance data are used to plot the accumulation of species with sampling effort. The resulting curve approaches an asymptotic maximum that can be estimated by extrapolation using the same approach as the Michaelis–Menten equation of enzyme kinetics (Nübel et al., 1999). This asymptote represents S_{max} , a theoretical species richness maximum (Colwell and Coddington, 1994). The S_{ACE} calculation, which is based on coverage, provides an estimate based on the relative number of species that occur only once, no more than 10 times, and more than 10 times (Chao et al., 1993; Kemp and Aller, 2004). It is considered to be more useful when some species occur more frequently. In contrast, S_{Chao1} takes into account the relative number of three classes: single species, those that appear twice, and the total number (Chao, 1984; Kemp and Aller, 2004). This may be more appropriate when most species are rare. Since each approach computes richness differently, estimates varied depending on the method used. In general, larger data sets yield estimates that are more precise and unbiased (Hughes et al., 2001), so microbial communities should be sampled extensively before any method is relied on exclusively. In this work, four different methods were utilized for comparative purposes to emphasize the uncertainty in species richness estimates.

2.7. Real-time quantitative PCR

Real-time Q-PCR experiments were designed to analyze the relative abundance of two 16S rDNA OTUs and one 18S rDNA OTU in three different samples using a Cepheid Smart Cycler system. The amount of fluorescent dye bound to each target OTU was measured over 40 cycles and compared among pelagic temperate lake samples. Individual 25 μl reactions included: 2.5 μl Takara 10 \times Ex TaqTM Buffer; 1.25 μl Takara dNTP Mixture (2.5 mM each); 1.25 μl SYBR[®] Green I nucleic acid gel stain (10 \times); 0.25 μl Takara Ex TaqTM; 1 μl OTU-specific forward and reverse primers (10 μM each); 16.75 μl sterile deionized H₂O; 1 μl experimental template (genomic DNA \sim 0.025 $\mu\text{g}/\mu\text{l}$), 1 μl positive control (mixed clone standard—25 pg/ μl each), or 1 μl negative control (sterile deionized H₂O). The mixed clone standard was prepared by combining three clones representing the three OTUs investigated. Relative abundance estimates were calculated using a 1:10 dilution series of the mixed clone standard to determine cycle number differences between 25, 2.5, 0.25, and 0.025 pg template concentrations.

3. Results

For each sample, libraries of SSU rDNA clones were produced, individual clones were randomly selected for sequencing, and sequences were aligned and sorted into OTUs. Rank abun-

dance curves for each sample showed some OTUs with multiple sequences, but most OTUs were represented by a single sequence (Fig. 1). When all 249 prokaryotic sequences were compiled, it was determined that 49 OTUs contained multiple clones and that 62 OTUs were unique, represented by only a single clone. An analysis of all eukaryotic sequences (250 clones) showed that 42 OTUs had multiple clones and that 67 OTUs were unique.

3.1. Sequence identification

The non-chimeric sequences were submitted for BLAST analysis to assess phylogenetic affiliations with sequences

reported in the GenBank database. If a sequence displayed <97.5% identity with all GenBank entries, it was considered to be novel and is described here as “unknown”. Thus, a sequence that displayed $\geq 97.5\%$ identity with a GenBank entry is referred to as “known,” even if the GenBank entry did not include a species identification. We found that the 97.5% identity threshold produced consistent results for sequences in the same OTU and that these OTUs generally corresponded to species-level units when the GenBank entry provided a species identification. The proportion of known OTUs was determined for each library (Table 2). The lowest proportion of known OTUs (25%) was found in the Lake Townsend spring sample and the highest proportion (48.6%) was found in Toolik

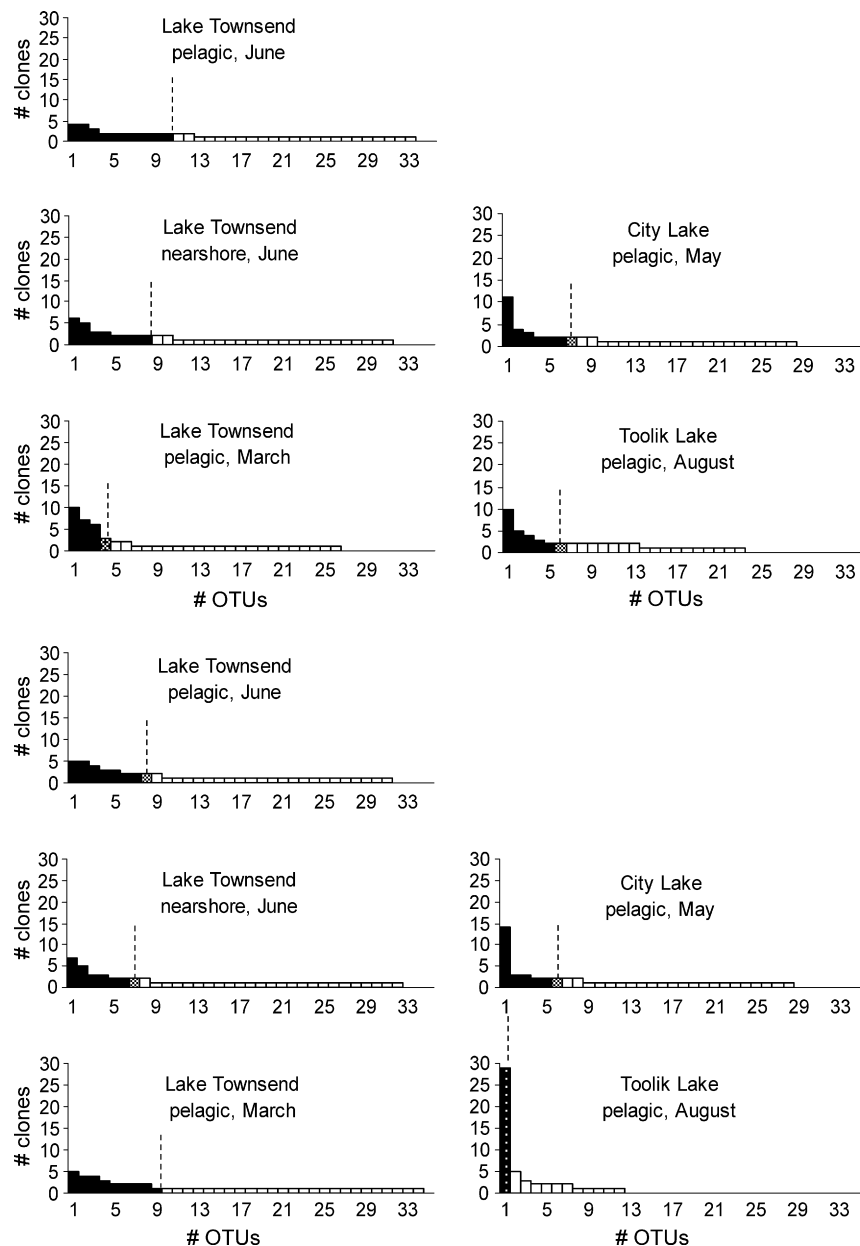


Fig. 1 – Rank-abundance curves for 16S rDNA libraries (upper panel) and 18S rDNA libraries (lower panel). Curves on left-hand side represent Lake Townsend samples. The median for each distribution partitions OTUs into two groups shown in black and white. When a median fell within an OTU, a stippled pattern was used to represent the relative proportion of sequences in each group.

Table 2 – BLAST analysis and diversity characteristics of sequenced prokaryotic and eukaryotic rDNA clones from water samples

	June			March			August		
	Lake Townsend pelagic,			Lake Townsend nearshore,			City Lake pelagic, May		
	June			June			August		
rDNA library	16S	18S	16S	16S	18S	16S	16S	18S	18S
Number of clones	50	50	50	50	50	49	50	50	50
Proportion of known clones (%) ^a	21/50 (42.0)	17/50 (34.0)	16/50 (32.0)	21/50 (42.0)	19/50 (38.0)	31/49 (63.3)	25/50 (50.0)	20/50 (40.0)	32/50 (64.0)
Number of OTUs	33	31	31	32	34	28	23	28	12
Proportion of known OTUs (%) ^b	12/33 (36.4)	8/31 (25.8)	10/31 (32.3)	8/32 (25.0)	9/34 (26.5)	13/28 (46.4)	14/23 (60.9)	6/28 (21.4)	3/12 (25.0)
Simpson index (evenness)	0.039	0.049	0.050	0.053	0.043	0.079	0.078	0.102	0.358
Shannon–Wiener diversity index	3.38	3.24	3.24	3.24	3.35	3.00	2.86	2.90	1.62

^a Proportion of known clones = proportion of clone sequences having $\geq 97.5\%$ similarity to sequences reported in GenBank.^b Proportion of known OTUs = proportion of OTUs with clone sequences having $\geq 97.5\%$ similarity to GenBank entries.

Lake. In general, the proportion of known 16S rDNA OTUs was higher than known 18S rDNA OTUs.

3.2. Species diversity

Measurements of species diversity differed among lakes (Table 2). Collectively, these measurements indicated that the temperate lakes have greater species diversity for prokaryotes and eukaryotes. Lake Townsend contained the most species and showed the most even OTU distribution. In contrast, richness estimates for Toolik Lake were the lowest, especially for eukaryotes, indicating that only a few competitors dominate the arctic community.

Rank-abundance curves illustrate diversity patterns. For the temperate lakes, these curves showed that few taxa appeared multiple times while many were represented by a single clone only, a trend indicating the presence of numerous species at low relative abundance (Fig. 1). In the arctic lake, fewer OTUs were recognized, but the number of sequences within some OTUs was relatively high. This implies either that fewer OTUs were present or that a larger proportion of the OTUs that were present were also rare, relative to the temperate samples. Estimates of total taxonomic diversity (Table 3) support this, and calculations suggest that sequenced clones in each sample recovered between one-third and two-thirds of the total number of species present, although results varied depending on the estimator used.

3.3. Library comparisons

Library comparisons were made to determine if similar estimates of species diversity indicated similar community composition. For each pairwise comparison, a similarity coefficient was calculated (Table 4) to quantify how many of the same OTUs appeared among the 50 clones characterized from each library. This analysis showed some overlap between every pair of samples, but the extent of commonality varied considerably. For example, no prokaryotic sequences were shared between one of the Lake Townsend summer samples and Toolik Lake, so their similarity is based only on overlapping eukaryotic OTUs. In other cases, roughly equal proportions of prokaryotes and eukaryotes were shared.

In addition, some comparisons indicated that shared OTUs are more likely to be identified sequences. Between the two Lake Townsend summer samples that were collected at the same time but at different locations, 16 of 63 eukaryotic OTUs were identified (25.8% in the Lake Townsend pelagic sample and 25% in the Lake Townsend nearshore sample) and three of these OTUs appeared in both samples. Thus, it appears that 60% of the eukaryotic taxa that were found in both places can be identified.

3.4. Library screening versus real-time Q-PCR

Several OTUs containing multiple clones appeared in only a single library. Three of these OTUs were used in fluorescence detection real-time PCR experiments to determine if they were also present in other genomic DNA samples from which clones had not been isolated (Fig. 2). Each OTU was detected in all of the samples investigated. The relative abundance of each OTU

Table 3 – Estimates of total species richness in prokaryotic and eukaryotic communities using four different methods

	Lake Townsend pelagic, June		Lake Townsend nearshore, June		Lake Townsend pelagic, March		City Lake pelagic, May		Toolik Lake pelagic, August	
rDNA library	16S	18S	16S	18S	16S	18S	16S	18S	16S	18S
Number of OTUs	33	31	31	32	26	34	28	28	23	12
S_{cov}	57	56	54	62	44	71	46	47	29	14
S_{max}	93	72	73	74	40	93	53	47	40	12
S_{ACE}	61	80	77	110	110	106	67	65	38	17
S_{Chao1}	54	77	63	88	91	99	54	60	28	14

was compared and estimated across the same three samples based on a dilution series of a known standard. According to cycle threshold differences between growth curves, the amount of the sequence identified as a cyanobacterial rDNA in the Lake Townsend spring sample was estimated to be 34× greater than the amount of this product in the Lake Townsend summer sample and 13× greater than the amount in City Lake. Similarly, for the sequence identified as *Zoogloea ramigera*, the amount of product in City Lake was about 41× greater than that found in the Lake Townsend spring sample and 219× greater than that found in the Lake Townsend summer sample. Finally, for the sequence identified as *Asterionella formosa*, the amount in the Lake Townsend spring sample was determined to be 29× more abundant than in the Lake Townsend summer sample and 55× more abundant than in City Lake.

4. Discussion

The objective of this study was to determine if partial profiles of microbial communities could be compared to make meaningful ecological inferences and to provide guidance in the development of environmental assays based on such profiles. To do so, we randomly drew a total of 100 clones from libraries of prokaryotic and eukaryotic SSU rDNA (50 clones from each) to identify the more common rDNA sequences from each sample. The underlying principal is that the community profile can act as a comprehensive bioindicator of water quality because microorganisms respond rapidly to environmental cues. The collection method yielded species diversity estimates that were consistent with expectations of the ecosystems studied. Further, the sensitivity of Q-PCR suggested that community differences were actually due to large variations in OTU abundance among samples, rather than the absence of OTUs from certain samples. This indicates that many microbial species are endemic to freshwater environments across great geographic distances and that local environmental variables control their abundance, not their existence, at specific sites across this range. These findings generally confirm the validity of this approach.

This study was not intended to assess species diversity rigorously, but we gained some insight by determining standard diversity measures that are often used to compare ecosystems (Table 2). For example, we found relatively high species richness for both prokaryotic and eukaryotic microbes. Diversity measures (Species Richness, Simpson's Index, Shannon–Wiener Index) yielded results consistent with expectations for the water bodies sampled. For example,

across a broad geographic scale, prokaryotic and eukaryotic diversity was lower in the oligotrophic arctic lake (Toolik Lake) than in either of the temperate systems. On a less extensive geographic scale, we generally found higher species diversity in mesotrophic Lake Townsend than in the more eutrophic City Lake. On a limited temporal scale, we found somewhat lower richness and diversity in the Lake Townsend spring sample than in the summer sample. Finally, we found that these patterns were generally similar for both prokaryotic and eukaryotic microbes. Although limited, these comparisons each meet with conventional expectations regarding diversity estimates.

Venn diagrams represent how OTUs were shared among lake samples (Fig. 3), illustrating the degree of similarity when different seasonal times and geographic locations were compared. A within-lake comparison of Lake Townsend (two summer samples, one spring sample) showed that three OTUs were shared (two prokaryotic OTUs, one eukaryotic OTU) with nearly equal representation in each library (Fig. 3A). A comparison between the two temperate lakes also showed three shared OTUs (Fig. 3B), including two prokaryotic OTUs and the same eukaryotic OTU that appeared in the Lake Townsend comparison. The comparison between all three lakes (Fig. 3C) revealed that one prokaryotic and one eukaryotic OTU were shared. Although different prokaryotic OTUs were shared in each case, the same shared eukaryotic OTU appeared in all three comparisons.

In fact, this OTU occurred in all five eukaryotic libraries and was identified as *Cryptomonas ovata*. This cosmopolitan appearance, via a collection method that was devised to recover the more common OTUs, indicates a broad tolerance range for this species. However, the relative abundance of *C. ovata* varied from sample to sample, appearing only once in Toolik Lake, four or five times in Lake Townsend samples, and 14 times in City Lake. This pattern of relative abundance follows a trend of increasingly eutrophic conditions.

OTUs found in all three lakes (Fig. 3C) were examined further to determine if population differences could be characterized. In some cases, an OTU showed patterns of sequence variation that appeared to differentiate lakes, possibly indicating the effects of local selective pressures. For example, one of the 16S rDNA OTUs contained two clones recovered from one of the Lake Townsend summer samples, three from City Lake, and three from Toolik Lake. Sequence alignments revealed eight variant nucleotide positions that distinguished temperate and arctic lake clones. At each of these positions, the temperate lake clones were identical and the arctic lake clones were identical, but none of the variant nucleotides were shared between these two groups (data not

Table 4 – Sorensen similarity coefficients resulting from prokaryotic and eukaryotic community comparisons

	Lake Townsend nearshore, June		Lake Townsend pelagic, March		City Lake pelagic, May		Toolik Lake pelagic, August	
rDNA library	16S	18S	16S	18S	16S	18S	16S	18S
Lake Townsend pelagic, June	1	1	0.344 (11)	0.169 (5)	0.230 (7)	0.068 (2)	0.071 (2)	0.093 (2)
Lake Townsend nearshore, June			1	0.070 (2)	0.169 (5)	0.133 (4)	0	0.091 (2)
Lake Townsend pelagic, March				1	0.161 (5)	0.122 (3)	0.174 (4)	0.200 (4)
City Lake pelagic, May					1	1	0.039 (1)	
Toolik Lake pelagic, August							1	1

Coefficients were calculated as follows: $S = 2C/(A + B)$, where A and B represent the number of OTUs in libraries A and B, and C represents the number of OTUs shared between A and B (McCaig et al., 1999; Odum, 1971). C is in () for each comparison.

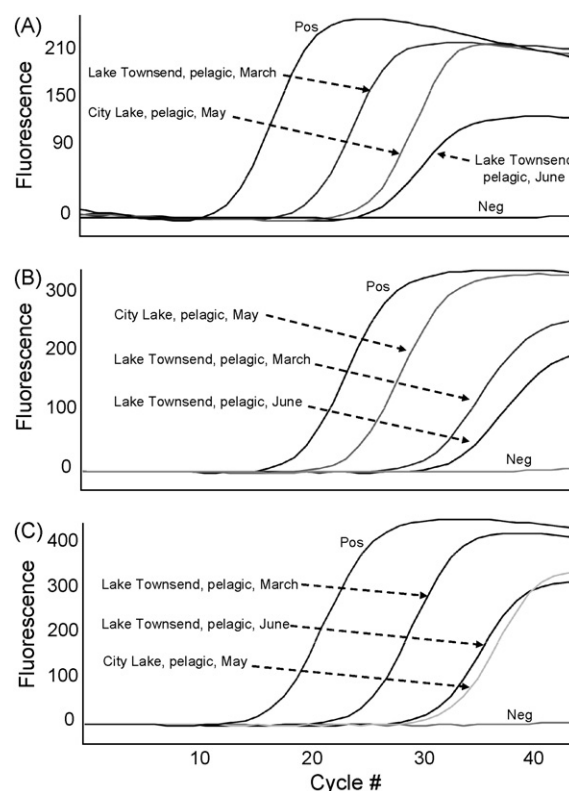


Fig. 2 – Q-PCR curves generated using OTU-specific primers and genomic DNA used to construct clone libraries. (A) Relative abundance of OTU aligning with unidentified cyanobacterium LD27 found only in the Lake Townsend March pelagic sample (10 of 50 16S rDNA sequences). (B) Relative abundance of OTU aligning with *Zoogloea ramigera* found only in the City Lake sample (11 of 50 16S rDNA sequences). (C) Relative abundance of OTU aligning with *Asterionella formosa*, which was found only in the Lake Townsend March pelagic sample (4 of 50 18S rDNA sequences). Pos, positive control; Neg, negative control.

shown). These single nucleotide distinctions within an OTU imply that such differences may be associated with different environmental conditions or geographical locales, creating the opportunity for indicator development within OTUs, as well as between OTUs.

Patterns of relative abundance among libraries are potentially important indicators of environmental differences. For example, one unknown prokaryotic OTU was found in all three lakes, but not in the library derived from the nearshore Lake Townsend sample. This unknown species appeared six times in the Lake Townsend spring library, the only one derived from a temperate sample collected in early spring, and it occurred only once in each of the other libraries. This pattern suggests an OTU that is better adapted to colder mesotrophic ecosystems. The same comparison also revealed a eukaryotic OTU, which had the most variable abundance. This sequence was recovered once from City Lake, five times from Lake Townsend in March, and 29 times from Toolik Lake. Thus, it likely represents a cold water adapted species. In fact, the OTU shows 99.5% sequence identity with *Leptodiatomus*

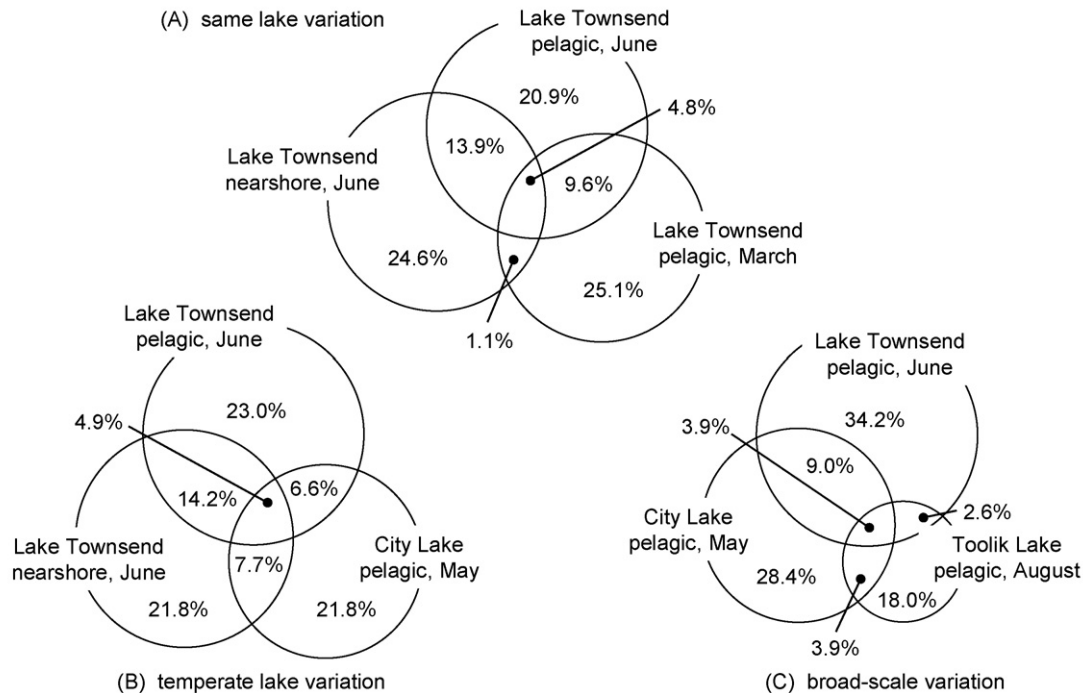


Fig. 3 – Venn diagrams showing relative patterns of shared microbial (prokaryotic + eukaryotic) OTUs. The size of each sample component is based on the total number of OTUs for that sample relative to the other samples.

coloradensis (GenBank accession number AY339152), a planktonic crustacean copepod, although this species may actually represent *Diaptomus* (*Leptodiaptomus*) *pribilofensis* since this is the only cold water diaptomid species detected so far in Toolik Lake (O'Brien et al., 1997).

Our results, and those of others (e.g. Kemp and Aller, 2004), consistently demonstrate rank abundance curves with long “tails” of rare taxa. It is clearly difficult to quantify actual microbial diversity in any system and exhaustive microbial inventories are not yet practical, so reliable estimators of natural diversity using available data are essential (Hughes et al., 2001; Curtis et al., 2002). Recent work by Venter et al. (2004) and Sogin et al. (2006) illustrate this challenge. Venter et al. (2004) used whole-genome shotgun sequencing to study Sargasso Sea microorganisms. They analyzed six gene sequences to predict species richness using various diversity estimators. Each gene sequence examined indicated a minimum of 300 species and more than 1000 species when combined. Sogin et al. (2006) used massive parallel sequencing (Margulies et al., 2005) to compare sequences of nearly 118,000 amplified PCR fragments of ribosomal genes in eight deep-water ocean samples. They found that each sample was dominated by a few species, but that thousands of rare species were also present.

Several recent papers review species richness estimators (e.g. Kemp and Aller, 2004) and estimates vary according to the estimator used. In our study, we compared four estimates of total species richness using different methods: S_{cov} , based on a simple coverage calculation; S_{max} , based on rarefaction analysis; the S_{ACE} and S_{Chao1} diversity estimators. Our results suggest that a limited sampling of 50 prokaryotic and 50

eukaryotic clones accounted for 25–50% of the total taxa present, except for the arctic lake libraries, which had much lower estimates of diversity and therefore represented a much higher percentage of estimated total taxa. Such calculations are tenuous, however, since rank abundance curves consistently show long tails of rare taxa, and accumulation curves frequently do not reach asymptotes (cf. Kemp and Aller, 2004; Countway et al., 2005).

Previous studies of prokaryotes and eukaryotes in Toolik Lake highlight this difficulty. Bahr et al. (1996) and Crump et al. (2003) used molecular approaches to census prokaryotic species in Toolik Lake and found a much greater diversity of taxa than indicated in this study. For eukaryotes, over 130 species of phytoplankton have been identified by direct microscopic observation, along with a number of ciliated protozoans and rotifers (O'Brien et al., 1997). Further, nanoflagellates are also common in Toolik, but have not been identified. In each of these studies, collection protocols were more extensive and multiple samples were analyzed to develop taxon lists.

Based on most of the rank abundance curves, we also note that our sampling regimen recovered a relatively small proportion of OTUs with multiple clones and a large proportion of rare individuals, many of which are represented by only a single clone. This observation is consistent with recent reports of a large “rare biosphere” of microbes in aquatic systems (Sogin et al., 2006). It follows that the resources necessary to extensively sample the taxa of any ecosystem using molecular tools would be prohibitive for routine assessments. However, this does not preclude the use of such tools for lake assessments, if comparisons can be achieved by characterizing the more common OTUs in a given sample.

Despite the limitations of a small sample size, our data suggest that even limited molecular assessments of aquatic systems can be used to characterize those systems for two reasons. First, we found both unique and common taxa in our sample libraries (Fig. 3). This result is consistent with the fact that microbes have varied tolerance ranges. For example, the chrysophyte *Cryptomonas ovata* was found frequently in each sample, while many OTUs, such as *Enterococcus gallinarum* HPC254 and *Didinium nasutum*, were found in only one sample. Second, the Q-PCR assays also showed that three OTUs were distributed much more widely than indicated by the library screenings (Fig. 2). This suggests that the relative abundance of individual OTUs, rather than simply differences in community OTU composition, may account for many of the differences observed among the microbial communities sampled. As applied to ecosystem assessments, it may be more effective, and practical, to quantify differences in species abundance, instead of relying on apparent species differences among samples.

The Q-PCR assays allowed for an estimation of the sensitivity of this approach in detecting community members. Based on four complete *E. coli* genomes (GenBank entries AE005174, AE014075, BA000007, and U00096) 16S rDNA comprises an average of about 0.206% of the *E. coli* genome, so ~52 pg of 16S rDNA can be expected to be present in 25 ng of genomic DNA material. Q-PCR methods resulted in the detection of a specific rDNA signal in genomic samples when as little as 3.6×10^{-3} pg of starting material was present, based on a comparison of fluorescent signals from genomic samples and signals from rDNA clones of known concentration used as positive controls. These calculations suggest that an extraordinarily large clone library would be required to ensure the recovery of such rare rDNAs by shotgun cloning.

Several studies have suggested that the widespread distribution of microbial taxa occurs because they are abundant, reproduce rapidly, and are easily dispersed (e.g. Finlay, 2002; Griffin et al., 2002; Fenchel, 2003). This idea has been supported by studies of aquatic systems (e.g. Zwart et al., 1998; Glöckner et al., 2000; Zwart et al., 2002), although there is also evidence that at least some extremophiles have much more restricted distributions (Papke et al., 2003; Whitaker et al., 2003). Our ability to detect three OTUs across lakes using Q-PCR, even at low abundance, is consistent with the idea of widespread species distribution.

In terms of indicator development, these results suggest that it is not necessary to extensively census a representative microbial community for every different combination of environmental characteristics. Instead, a single comprehensive suite of microorganisms could operate as a bioindicator for any environmental assessment, simply by noting patterns of relative abundance and associating these patterns with local environmental conditions. Since microorganisms that are rare in one environment may be much more common in another, the development of a comprehensive suite could be accomplished by modestly sampling several libraries derived from well-selected sites over time to recover sufficient microbial diversity. During the development process, Q-PCR experiments could be used in parallel as a validation tool to detect rare rDNAs and measure quantitative differences between samples. Only robust rDNAs that produce reliable

data would become part of the community profile used as an indicator for environmental assessments.

As metagenomic profiles are being developed and interpreted, a variety of technical concerns must be considered, including DNA extraction and PCR biases (e.g. Liesack et al., 1991; Reysenbach et al., 1992; Haldeman et al., 1994; Chandler et al., 1997), the sampling effort required to characterize diversity sufficiently (e.g. Hughes et al., 2001; Kemp and Aller, 2004), and accurate identification of unknown taxa (e.g. Kroes et al., 1999; McCaig et al., 1999; Suau et al., 1999). Clearly, the diversity of OTUs recovered from amplification libraries depends on PCR conditions. Nevertheless, several observations suggest the validity of the data reported here. First, the more common OTUs varied in their relative abundance among the five samples, strongly suggesting that their frequency reflects sample differences rather than amplification bias. Second, some OTUs were recovered multiple times from one library, while not at all from other libraries, thus discounting the likelihood that PCR biases explain the recovery of these OTUs. Third, the recovery of chimeric clones was low (0.02%), suggesting that amplification artifacts were minimal. Q-PCR using primers intended to be OTU-specific revealed tremendous differences in abundance for a given OTU among the genomic samples. In these cases, the OTU was always detected in greatest abundance in the genomic sample which had yielded the clone. Finally, single nucleotide variation at various sites within OTUs, although not examined extensively in this study, suggests that microdiversity is an important feature of community organization (Acinas et al., 2004; Fawley et al., 2004).

The results of this study suggest that metagenomic profiling can be used to characterize ecosystems. Although there is still much to be learned about the difficulties of adequately sampling diverse ecosystems, effectively quantifying results, and optimizing methodologies, it is evident that microbial communities can tell us much about the state of aquatic ecosystems. As the bioindicator potential of aquatic microbial communities is elucidated, application of this knowledge through methods such as microarrays should provide useful tools for research, regulatory agencies, and industry.

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